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PATENT APPLICATION: US/10/018,030

DATE: 01/09/2002

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3 <110> APPLICANT: Searfoss III, George H.  
 4 Pagnoni, Marco F.  
 5 Ivashchenko, Yuri D.  
 6 Guo, Kun  
 7 Clark, Kenneth L.  
 9 <120> TITLE OF INVENTION: VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF  
 10 TNF-ALPHA (TNFa) SIGNALING PATHWAY  
 12 <130> FILE REFERENCE: 22816 PCT  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/018,030  
 C--> 15 <141> CURRENT FILING DATE: 2001-10-23  
 17 <150> PRIOR APPLICATION NUMBER: 60/131940  
 18 <151> PRIOR FILING DATE: 1999-04-30  
 20 <160> NUMBER OF SEQ ID NOS: 5  
 22 <170> SOFTWARE: PatentIn Ver. 2.0  
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 26 <212> TYPE: DNA  
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 32 ctccgcaggc ccttcaggc gcagtgtggc caccggtaact gctccttctg cctggccagc 180  
 33 atcctcagct ctgggcctca gaactgtgct gcctgtgttc acgagggcat atatgaagaa 240  
 34 ggcatttcta ttttagaaag cagttcggcc tccccagata atgctgcccg cagggagggtg 300  
 35 gagagcctgc cggccgtctg tcccagtgat ggatgcacct ggaaggggac cctgaaagaa 360  
 36 tacgagtttc aggaccacgt caagacttgt ggcaagtgtc gagtcccttg cagattccac 420  
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 42 aaggtgcagc agctggagag gagcattggc ctcaaggacc tggcgatggc tgacttggag 780  
 43 cagaaggtct tggagatgga ggcattccacc tacgatggg tcttcatctg gaagatctca 840  
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 45 gccttctaca ccagcaggta cggctacaag atgtgtctgc gtatctacct gaacggcgac 960  
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 47 gccctgctgc ggtggccctt caaccagaag gtgaccttaa tgctgctcga ccagaataac 1080  
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66              35              40              45
68 Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Ala Ser Ile Leu Ser Ser
69              50              55              60
71 Gly Pro Gln Asn Cys Ala Ala Cys Val His Glu Gly Ile Tyr Glu Glu
72 65              70              75              80
74 Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala Phe Pro Asp Asn Ala Ala
75              85              90              95
77 Arg Arg Glu Val Glu Ser Leu Pro Ala Val Cys Pro Ser Asp Gly Cys
78              100             105             110
80 Thr Trp Lys Gly Thr Leu Lys Glu Tyr Glu Phe Gln Asp His Val Lys
81              115             120             125
83 Thr Cys Gly Lys Cys Arg Val Pro Cys Arg Phe His Ala Ile Gly Cys
84              130             135             140
86 Leu Glu Thr Val Glu Gly Glu Lys Gln Gln Glu His Glu Val Gln Trp
87 145             150             155             160
89 Leu Arg Glu His Leu Ala Met Leu Leu Ser Ser Val Leu Glu Ala Lys
90              165             170             175
92 Pro Leu Leu Gly Asp Gln Ser His Ala Gly Ser Glu Leu Leu Gln Arg
93              180             185             190
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96              195             200             205
98 Val Leu Asn Arg Glu Val Glu Arg Val Ala Met Thr Ala Glu Ala Cys
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101 Ser Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu Ala Leu Ser Ser
102 225             230             235             240
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108              260             265             270
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111              275             280             285
113 Ala Val Ala Gly Arg Ile Pro Ala Ile Phe Ser Pro Ala Phe Tyr Thr
114              290             295             300
116 Ser Arg Tyr Gly Tyr Lys Met Cys Leu Arg Ile Tyr Leu Asn Gly Asp
117 305             310             315             320
119 Gly Thr Gly Arg Gly Thr His Leu Ser Leu Phe Phe Val Val Met Lys
120              325             330             335
122 Gly Pro Asn Asp Ala Leu Leu Arg Trp Pro Phe Asn Gln Lys Val Thr
123              340             345             350
125 Leu Met Leu Leu Asp Gln Asn Asn Arg Glu His Val Ile Asp Ala Phe
126              355             360             365
128 Arg Pro Asp Val Thr Ser Ser Ser Phe Gln Arg Pro Val Asn Asp Met
129              370             375             380
131 Asn Ile Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu
132 385             390             395             400

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138                               420
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149 gtcaagactt gtggcaagtg tcgagtcctt tgcagattcc acgccatcgg ctgcctcgag 180
150 acggtagagg gtgagaaaca gcaggagcac gaggtgcagt ggctgcggga gcacctggcc 240
151 atgctactga gctcggtgct ggaggcaaag cccctcttgg gagaccagag ccacgcgggg 300
152 tcagagctcc tgcagaggtg cgagagcctg gagaagaaga cggccacttt tgagaacatt 360
153 gtctgcgtcc tgaaccggga ggtggagagg gtggccatga ctgccgaggc ctgcagccgg 420
154 cagcaccggc tggaccaaga caagattgaa gccctgagta gcaaggtgca gcagctggag 480
155 aggagcattg gcctcaagga cctggcgatg gctgacttgg agcagaaggt cttggagatg 540
156 gaggcatcca cctacgatgg ggtcttcac tgggaagatc cagacttcgc caggaagctc 600
157 caggaagctg tggctggccg cataccgcc atcttctccc cagccttcta caccagcagg 660
158 tacggctaca agatgtgtct gcgtatctac ctgaacggcg acggcaccgg gcgaggaaca 720
159 cacctgtccc tcttctttgt ggtgatgaag ggcccgaatg acgccctgct gcggtggccc 780
160 ttcaaccaga aggtgacctt aatgctgctc gaccagaata accgggagca cgtgattgac 840
161 gccttcaggc ccgacgtgac ttcactctt ttccagaggc cagtcaacga catgaacatc 900
162 gcaagcggct gccccctctt ctgccccgtc tccaagatgg aggcaaagaa ttcctacgtg 960
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174 Leu Pro Ala Val Cys Pro Ser Asp Gly Cys Thr Trp Lys Gly Thr Leu
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177 Lys Glu Tyr Glu Phe Gln Asp His Val Lys Thr Cys Gly Lys Cys Arg
178 35 40 45
180 Val Pro Cys Arg Phe His Ala Ile Gly Cys Leu Glu Thr Val Glu Gly
181 50 55 60
183 Glu Lys Gln Gln Glu His Glu Val Gln Trp Leu Arg Glu His Leu Ala
184 65 70 75 80
186 Met Leu Leu Ser Ser Val Leu Glu Ala Lys Pro Leu Leu Gly Asp Gln
187 85 90 95
189 Ser His Ala Gly Ser Glu Leu Leu Gln Arg Cys Glu Ser Leu Glu Lys
190 100 105 110
192 Lys Thr Ala Thr Phe Glu Asn Ile Val Cys Val Leu Asn Arg Glu Val
193 115 120 125
195 Glu Arg Val Ala Met Thr Ala Glu Ala Cys Ser Arg Gln His Arg Leu
196 130 135 140

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201 Arg Ser Ile Gly Leu Lys Asp Leu Ala Met Ala Asp Leu Glu Gln Lys
202                      165                      170                      175
204 Val Leu Glu Met Glu Ala Ser Thr Tyr Asp Gly Val Phe Ile Trp Lys
205                      180                      185                      190
207 Ile Ser Asp Phe Ala Arg Lys Leu Gln Glu Ala Val Ala Gly Arg Ile
208                      195                      200                      205
210 Pro Ala Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg Tyr Gly Tyr Lys
211                      210                      215                      220
213 Met Cys Leu Arg Ile Tyr Leu Asn Gly Asp Gly Thr Gly Arg Gly Thr
214 225                      230                      235                      240
216 His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro Asn Asp Ala Leu
217                      245                      250                      255
219 Leu Arg Trp Pro Phe Asn Gln Lys Val Thr Leu Met Leu Leu Asp Gln
220                      260                      265                      270
222 Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro Asp Val Thr Ser
223                      275                      280                      285
225 Ser Ser Phe Gln Arg Pro Val Asn Asp Met Asn Ile Ala Ser Gly Cys
226                      290                      295                      300
228 Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala Lys Asn Ser Tyr Val
229 305                      310                      315                      320
231 Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile Val Asp Leu Thr Gly Leu
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238 &lt;210&gt; SEQ ID NO: 5

239 &lt;211&gt; LENGTH: 2262

240 &lt;212&gt; TYPE: DNA

241 &lt;213&gt; ORGANISM: Homo sapiens

243 &lt;220&gt; FEATURE:

244 &lt;221&gt; NAME/KEY: misc\_feature

245 &lt;222&gt; LOCATION: ( )..)

246 <223> OTHER INFORMATION: TRAF2 truncated sequence contains an internal  
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249 &lt;400&gt; SEQUENCE: 5

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252 ctccctggga ccaagctgga agccaagtac ctgtgctccg cctgcagaaa cgtcctccgc 180
253 aggcccttcc aggcgcagtg tggccaccgg tactgtcctt tctgcctggc cagcatcctc 240
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262 tgctctgaga cggtagaggg tgagaaacag caggagcacg aggtgcagtg gctgcgggag 780
263 cacctggcca tgctactgag ctcggtgctg gaggcaaagc ccctcttggg agaccagagc 840
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VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date